W. Lagar-Wesley

1812

Serial Number: 08/943,776

CRF Processing Date: 1/5/98
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☑ Deleted *ending* stop codon in amino acid sequences ~~and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug)~~. Sequences corrected: Seq 2 _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

ENTERED

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT: Degli-Esposti, Mariapia
 6                        Goodwin, Raymond
 7
 8        (ii) TITLE OF INVENTION: Novel Receptor That Causes Cell Death
 9
10       (iii) NUMBER OF SEQUENCES: 6
11
12        (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: Immunex
14              (B) STREET: 51 University Street
15              (C) CITY: Seattle
16              (D) STATE: WA
17              (E) COUNTRY: USA
18              (F) ZIP: 98101
19
20         (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Floppy disk
22              (B) COMPUTER: Apple Power Macintosh
23              (C) OPERATING SYSTEM: Apple Operating System 7.5.3
24              (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
25
26        (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER:
28              (B) FILING DATE:   03 OCTOBER 1997
29              (C) CLASSIFICATION:
30
31       (vii) PRIOR APPLICATION DATA:
32              (A) APPLICATION NUMBER: USSN 60/044,456
33              (B) FILING DATE:   04 OCTOBER 1996
34              (C) CLASSIFICATION:
35
36      (viii) ATTORNEY/AGENT INFORMATION:
37              (A) NAME: Perkins, Patricia Anne
38              (B) REGISTRATION NUMBER: 34,693
39              (C) REFERENCE/DOCKET NUMBER: 2849-A
40
41        (ix) TELECOMMUNICATION INFORMATION:
42              (A) TELEPHONE: 2065870430
43
44
45    (2) INFORMATION FOR SEQ ID NO:1:
46
```

```
47          (i) SEQUENCE CHARACTERISTICS:
48              (A) LENGTH: 1847 base pairs
49              (B) TYPE: nucleic acid
50              (C) STRANDEDNESS: single
51              (D) TOPOLOGY: Not Relevant
52
53         (ii) MOLECULE TYPE: cDNA
54
55        (iii) HYPOTHETICAL: NO
56
57         (iv) ANTI-SENSE: NO
58
59        (vii) IMMEDIATE SOURCE:
60              (B) CLONE: AIR
61
62         (ix) FEATURE:
63              (A) NAME/KEY: CDS
64              (B) LOCATION: 236..1489
65
66         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67   CTTTTCAGCC ATACCCGGAT GGTTCTGTCC TCGCTGGCCG TGATCACGCC GTCCTCCTTG   60
68
69   GGGATGAGCA GCGCGGCCGT GACGGCGTCC TGGTGCCCCT CGATCTTGCT CAGCAGCACC  120
70
71   GGGCGGCTGC TCTGCGGCCT GGAGTGGATT TCGGCCGCCA TGTTCGCGCG GCGACTGCTG  180
72
73   CGGCCTCCTC GGCAGGCAGC CCATCAGCTG ACGCCTGGGC GCCCGTCGGA GGGCT ATG   238
74                                                             Met
75                                                               1
76
77   GAG CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC CTC CTG   286
78   Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu Leu
79                5               10               15
80
81   GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT CGT AGC CCC AGG TGT   334
82   Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg Cys
83           20               25               30
84
85   GAC TGT GCC GGT GAC TTC CAC AAG AAG ATT GGT CTG TTT TGT TGC AGA   382
86   Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys Arg
87       35               40               45
88
89   GGC TGC CCA GCG GGG CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC   430
90   Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys
91    50               55               60               65
92
93   GGC AAC TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC TGG   478
94   Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala Trp
95                70               75               80
96
97   GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG GCC TGT GAT GAG   526
98   Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp Glu
99                85               90               95
```

INPUT SET: S22359.raw

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100
101   CAG GCC TCC CAG GTG GCG CTG GAG AAC TGT TCA GCA GTG GCC GAC ACC   574
102   Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp Thr
103           100                 105                 110
104
105   CGC TGT GGC TGT AAG CCA GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA   622
106   Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser Gln
107           115                 120                 125
108
109   TGT GTC AGC AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG   670
110   Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly
111   130                 135                 140                 145
112
113   GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA GAT ACT GAC   718
114   Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp
115               150                 155                 160
116
117   TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA CAT GGC GAT GGC TGC GTG   766
118   Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val
119               165                 170                 175
120
121   TCC TGC CCC ACG AGC ACC CTG GGG AGC TGT CCA GAG CGC TGT GCC GCT   814
122   Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala
123               180                 185                 190
124
125   GTC TGT GGC TGG AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC   862
126   Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly
127           195                 200                 205
128
129   CTT GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA TAC CGC   910
130   Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg
131   210                 215                 220                 225
132
133   CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA GAT GAA GCT GGG ATG   958
134   His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly Met
135               230                 235                 240
136
137   GAG GCT CTG ACC CCA CCA CCG GCC ACC CAT CTG TCA CCC TTG GAC AGC   1006
138   Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp Ser
139               245                 250                 255
140
141   GCC CAC ACC CTT CTA GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC   1054
142   Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr
143               260                 265                 270
144
145   GTC CAG TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC CAG   1102
146   Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr Gln
147           275                 280                 285
148
149   GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC CAG TTG CCC AGC   1150
150   Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro Ser
151   290                 295                 300                 305
152
```

INPUT SET: S22359.raw

```
153   AGA GCT CTT GGC CCC GCT GCT GCG CCC ACA CTC TCG CCA GAG TCC CCA   1198
154   Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser Pro
155                   310                 315                 320
156
157   GCC GGC TCG CCA GCC ATG ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC   1246
158   Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp
159                   325                 330                 335
160
161   GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG   1294
162   Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr
163                   340                 345                 350
164
165   CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC GGC   1342
166   Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile Gly
167           355                 360                 365
168
169   CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG CAG   1390
170   Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln
171   370                 375                 380                 385
172
173   CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG GGG   1438
174   Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly
175                   390                 395                 400
176
177   CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG   1486
178   Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
179                   405                 410                 415
180
181   TGA CACGGCGCCC ACTTGCCACC TAGGCGCTCT GGTGGCCCTT GCAGAAGCCC       1539
182   *
183
184   TAAGTACGGT TACTTATGCG TGTAGACATT TTATGTCACT TATTAAGCCG CTGGCACGGC   1599
185
186   CCTGCGTAGC AGCACCAGCC GGCCCCACCC CTGCTCGCCC CTATCGCTCC AGCCAAGGCG   1659
187
188   AAGAAGCACG AACGAATGTC GAGAGGGGGT GAAGACATTT CTCAACTTCT CGGCCGGAGT   1719
189
190   TTGGCTGAGA TCGCGGTATT AAATCTGTGA AAGAAAACAA AAAAAAAAAA ACCGGAATTC   1779
191
192   GATATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGC CCGGTACCCA ATTCGCCCTA   1839
193
194   TAGTGAGT                                                          1847
195
196
197   (2) INFORMATION FOR SEQ ID NO:2:
198
199           (i) SEQUENCE CHARACTERISTICS:
200                   (A) LENGTH: 417 amino acids
201                   (B) TYPE: amino acid
202                   (D) TOPOLOGY: linear
203
204           (ii) MOLECULE TYPE: protein
205
```

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/943,776*

INPUT SET: S22359.raw

```
206          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
207
208     Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
209      1               5              10               15
210
211     Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
212              20              25               30
213
214     Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
215          35              40               45
216
217     Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
218          50              55               60
219
220     Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
221      65              70               75               80
222
223     Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
224                      85               90               95
225
226     Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
227              100             105             110
228
229     Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
230              115             120             125
231
232     Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
233          130             135             140
234
235     Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
236      145             150             155             160
237
238     Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
239              165             170             175
240
241     Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala
242              180             185             190
243
244     Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala
245          195             200             205
246
247     Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
248          210             215             220
249
250     Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
251      225             230             235             240
252
253     Met Glu Ala Leu Thr Pro Pro Ala Thr His Leu Ser Pro Leu Asp
254              245             250             255
255
256     Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
257              260             265             270
258
```

PAGE: 6

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/943,776*

DATE: 01/06/98
TIME: 10:41:22

INPUT SET: S22359.raw

****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

```
197    (2) INFORMATION FOR SEQ ID NO:2:
198
199            (i) SEQUENCE CHARACTERISTICS:
200                    (A) LENGTH: 417 amino acids
201                    (B) TYPE: amino acid
202                    (D) TOPOLOGY: linear
203
204            (ii) MOLECULE TYPE: protein
205
206            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
207
208    Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
209     1           5                   10                  15
210
211    Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
212                 20                  25                  30
213
214    Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
215             35                  40                  45
216
217    Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
218         50                  55                  60
219
220    Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
221     65                  70                  75                  80
222
223    Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
224                 85                  90                  95
225
226    Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
227                 100                 105                 110
228
229    Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
230             115                 120                 125
231
232    Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
233             130                 135                 140
234
235    Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
236    145                 150                 155                 160
237
238    Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
239                 165                 170                 175
240
241    Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala
242             180                 185                 190
243
```

RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/943,776

INPUT SET: S22359.raw

```
244   Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala
245       195             200             205
246
247   Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
248       210             215             220
249
250   Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
251   225             230             235             240
252
253   Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
254               245             250             255
255
256   Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
257           260             265             270
258
259   Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
260       275             280             285
261
262   Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
263       290             295             300
264
265   Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
266   305             310             315             320
267
268   Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
269               325             330             335
270
271   Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
272               340             345             350
273
274   Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile
275       355             360             365
276
277   Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln
278       370             375             380
279
280   Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
281   385             390             395             400
282
283   Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
284               405             410             415
285
286   Pro
287
288
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/943,776*

INPUT SET: S22359.raw

Line	Error	Original Text

1812

PAGE: 1
RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/943,776*
DATE: 01/05/98
TIME: 14:55:49

INPUT SET: S22359.raw

This Raw Listing contains ⌐G⌐
Information Section and ⌐
containing ERRORS.

Corrected Diskette Needed
Does Not Comply

```
 1                                      SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5        (i) APPLICANT: Degli-Esposti, Mariapia
 6                       Goodwin, Raymond
 7
 8       (ii) TITLE OF INVENTION: Novel Receptor That Causes Cell Death
 9
10      (iii) NUMBER OF SEQUENCES: 6
11
12       (iv) CORRESPONDENCE ADDRESS:
13             (A) ADDRESSEE: Immunex
14             (B) STREET: 51 University Street
15             (C) CITY: Seattle
16             (D) STATE: WA
17             (E) COUNTRY: USA
18             (F) ZIP: 98101
19
20        (v) COMPUTER READABLE FORM:
21             (A) MEDIUM TYPE: Floppy disk
22             (B) COMPUTER: Apple Power Macintosh
23             (C) OPERATING SYSTEM: Apple Operating System 7.5.3
24             (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
25
26       (vi) CURRENT APPLICATION DATA:
27             (A) APPLICATION NUMBER:
28             (B) FILING DATE:   03 OCTOBER 1997
29             (C) CLASSIFICATION:
30
31      (vii) PRIOR APPLICATION DATA:
32             (A) APPLICATION NUMBER: USSN 60/044,456
33             (B) FILING DATE:   04 OCTOBER 1996
34             (C) CLASSIFICATION:
35
36     (viii) ATTORNEY/AGENT INFORMATION:
37             (A) NAME: Perkins, Patricia Anne
38             (B) REGISTRATION NUMBER: 34,693
39             (C) REFERENCE/DOCKET NUMBER: 2849-A
40
41       (ix) TELECOMMUNICATION INFORMATION:
42             (A) TELEPHONE: 2065870430
43
44
```

ERRORED SEQUENCES FOLLOW:

08/943,776

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 417 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu
1               5               10              15

Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg
            20              25              30

Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys
        35              40              45

Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro
    50              55              60

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
65              70              75              80

Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
            85              90              95

Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
        100             105             110

Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
    115             120             125

Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
    130             135             140

Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
145             150             155             160

Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
            165             170             175

Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala
            180             185             190

Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala
            195             200             205

Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
210             215             220

Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
225             230             235             240

Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
            245             250             255

Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
```

```
                260                      265                      270
Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
        275                  280                  285

Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
        290                  295                  300

Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
305                  310                  315                  320

Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
                325                  330                  335

Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
                340                  345                  350

Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile
        355                  360                  365

Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln
        370                  375                  380

Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met
385                  390                  395                  400

Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly
                405                  410                  415
Pro
```

Pro *(★) delete*